FIGURE 1

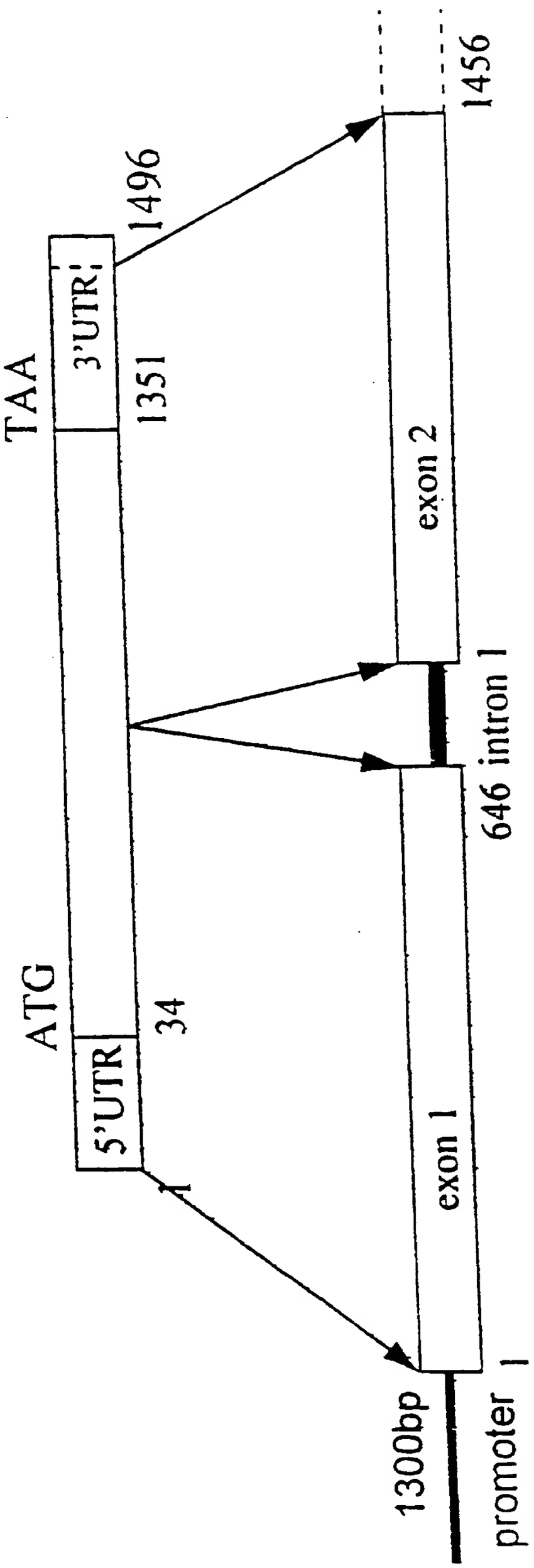


FIGURE 2

```
                          10         20         30         40         50
MOUSE-X1.DNA       1 ATGAGGCTTC CTGGTTGGTT GTGGCTGAGT TCTGCCGTCC TCGCTGCCTG      50
HUMAN-X1.DNA       1 ATGAAGCTGG CTAACTGGTA CTGGCTGAGC TCAGCTGTTC TTGCCACTTA      50
                          60         70         80         90        100
MOUSE-X1.DNA      51 CCGAGC---G GTGGAGGAGC ACAACCTGAC TGAGGGGCTG GAGGATGCCA     100
HUMAN-X1.DNA      51 CGGTTTTTTG GTTGTGGCAA ACAATGAAAC AGAGGAAATT AAAGATGAAA     100
                         110        120        130        140        150
MOUSE-X1.DNA     101 GCGCCCAGGC TGCCTGCCCC GCGAGGCTGG AGGGCAGCGG GAGGTGCGAG     150
HUMAN-X1.DNA     101 GAGCAAAGGA TGTCTGCCCA GTGAGACTAG AAAGCAGAGG GAAATGCGAA     150
                         160        170        180        190        200
MOUSE-X1.DNA     151 GGGA---GCC AGTGCCCCTT CCAGCTCACC CTGCCCACGC TGACCATCCA     200
HUMAN-X1.DNA     151 GAGGCAGGGG AGTGCCCCTA CCAGGTAAGC CTGCCCCCCT TGACTATTCA     200
                         210        220        230        240        250
MOUSE-X1.DNA     201 GCTCCCGCGG CAGCTTGGCA GCATGGAGGA GGTGCTCAAA GAAGTGCGGA     250
HUMAN-X1.DNA     201 GCTCCCGAAG CAATTCAGCA GGATCGAGGA GGTGTTCAAA GAAGTCCAAA     250
                         260        270        280        290        300
MOUSE-X1.DNA     251 CCCTCAAGGA AGCAGTGGAC AGTCTGAAGA AATCCTGCCA GGACTGTAAG     300
HUMAN-X1.DNA     251 ACCTCAAGGA AATCGTAAAT AGTCTAAAGA AATCTTGCCA AGACTGCAAG     300
                         310        320        330        340        350
MOUSE-X1.DNA     301 TTGCAGGCTG ACGACCATCG AGATCCCGGC GGGAATGGAG GG--------     350
HUMAN-X1.DNA     301 CTGCAGGCTG ATGACAACGG AGACCCAGGC AGAAACGGAC TGTTGTTACC     350
                         360        370        380        390        400
MOUSE-X1.DNA     351 -AAT---GGA GC---AGAGA CAGCCGAGGA CAGTAGAGTC CAGGAACTGG     400
HUMAN-X1.DNA     351 CAGTACAGGA GCCCCGGGAG AGGTTGGTGA TAACAGAGTT AGAGAATTAG     400
                         410        420        430        440        450
MOUSE-X1.DNA     401 AGAGTCAGGT GAACAAGCTG TCCTCAGAGC TGAAGAATGC AAAGGACCAG     450
HUMAN-X1.DNA     401 AGAGTGAGGT TAACAAGCTG TCCTCTGAGC TAAAGAATGC CAAAGAGGAG     450
                         460        470        480        490        500
MOUSE-X1.DNA     451 ATCCAGGGGC TGCAGGGGCG CCTGGAGACG CTCCATCTGG TAAATATGAA     500
HUMAN-X1.DNA     451 ATCAATGTAC TTCATGGTCG CCTGGAGAAG CTGAATCTTG TAAATATGAA     500
                         510        520        530        540        550
MOUSE-X1.DNA     501 CAACATTGAG AACTACGTGG ACAACAAAGT GGCAAATCTA ACCGTTGTGG     550
HUMAN-X1.DNA     501 CAACATAGAA AATTATGTTG ACAGCAAAGT GGCAAATCTA ACATTTGTTG     550
                         560        570        580        590        600
MOUSE-X1.DNA     551 TCAACAGTTT GGATGGCAAG TGTTCCAAGT GTCCCAGCCA AGAACACATG     600
HUMAN-X1.DNA     551 TCAATAGTTT GGATGGCAAA TGTTCAAAGT GTCCCAGCCA AGAACAAATA     600
                         610        620        630        640        650
MOUSE-X1.DNA     601 CAGTCACAGC CGG....... .......... .......... ..........     650
HUMAN-X1.DNA     601 CAGTCACGTC CAG....... .......... .......... ..........     650
```

FIGURE 3

```
                          10         20         30         40         50
MOUSE-X2.DNA       1 TTCAACATCT AATATACAAA GATTGTTCCG ACCACTACGT GCTAGGAAGG      50
HUMAN-X2.DNA       1 TTCAACATCT AATATATAAA GATTGCTCTG ACTACTACGC AATAGGCAAA      50
                          60         70         80         90        100
MOUSE-X2.DNA      51 AGAAGCAGTG GGGCCTACAG AGTTACCCCT GATCACAGAA ACAGCAGCTT     100
HUMAN-X2.DNA      51 AGAAGCAGTG AGACCTACAG AGTTACACCT GATCCCAAAA ATAGTAGCTT     100
                         110        120        130        140        150
MOUSE-X2.DNA     101 TGAGGTCTAC TGTGACATGG AGACCATGGG TGGAGGCTGG ACGGTGCTGC     150
HUMAN-X2.DNA     101 TGAAGTTTAC TGTGACATGG AGACCATGGG GGGAGGCTGG ACAGTGCTGC     150
                         160        170        180        190        200
MOUSE-X2.DNA     151 AGGCTCGCCT TGATGGCAGC ACCAACTTCA CCAGAGAGTG GAAAGACTAC     200
HUMAN-X2.DNA     151 AGGCACGTCT CGATGGGAGC ACCAACTTCA CCAGAACATG GCAAGACTAC     200
                         210        220        230        240        250
MOUSE-X2.DNA     201 AAAGCCGGCT TTGGAAACCT TGAACGAGAA TTTTGGTTGG GCAACGATAA     250
HUMAN-X2.DNA     201 AAAGCAGGCT TTGGAAACCT CAGAAGGGAA TTTTGGCTGG GGAACGATAA     250
                         260        270        280        290        300
MOUSE-X2.DNA     251 AATTCATCTT CTGACCAAGA GTAAGGAAAT GATTTTGAGA ATAGATCTTG     300
HUMAN-X2.DNA     251 AATTCATCTT CTGACCAAGA GTAAGGAAAT GATTCTGAGA ATAGATCTTG     300
                         310        320        330        340        350
MOUSE-X2.DNA     301 AAGACTTTAA TGGTCTCACA CTTTATGCCT TGTATGATCA GTTTTATGTG     350
HUMAN-X2.DNA     301 AAGACTTTAA TGGTGTCGAA CTATATGCCT TGTATGATCA GTTTTATGTG     350
                         360        370        380        390        400
MOUSE-X2.DNA     351 GCTAATGAAT TTCTCAAATA CCGATTACAC ATCGGTAACT ACAATGGCAC     400
HUMAN-X2.DNA     351 GCTAATGAGT TTCTCAAATA TCGTTTACAC GTTGGTAACT ATAATGGCAC     400
                         410        420        430        440        450
MOUSE-X2.DNA     401 GGCAGGGGAT GCCTTGCGTT TCAGTCGACA CTACAACCAT GACCTGAGGT     450
HUMAN-X2.DNA     401 AGCTGGAGAT GCATTACGTT TCAACAAACA TTACAACCAC GATCTGAAGT     450
                         460        470        480        490        500
MOUSE-X2.DNA     451 TTTTCACAAC CCCAGACAGA GACAACGATC GGTACCCCTC TGGGAACTGT     500
HUMAN-X2.DNA     451 TTTTCACCAC TCCAGATAAA GACAATGATC GATATCCTTC TGGGAACTGT     500
                         510        520        530        540        550
MOUSE-X2.DNA     501 GGGCTCTATT ACAGCTCAGG CTGGTGGTTT GATTCATGTC TCTCTGCCAA     550
HUMAN-X2.DNA     501 GGGCTGTACT ACAGTTCAGG CTGGTGGTTT GATGCATGTC TTTCTGCAAA     550
                         560        570        580        590        600
MOUSE-X2.DNA     551 CTTAAATGGC AAATATTACC ACCAGAAATA CAAAGGTGTC CGTAATGGGA     600
HUMAN-X2.DNA     551 CTTAAATGGC AAATATTATC ACCAAAAATA CAGAGGTGTC CGTAATGGGA     600
                         610        620        630        640        650
MOUSE-X2.DNA     601 TTTTCTGGGG CACCTGGCCT GGTATAAACC AGGCACAGCC AGGTGGCTAC     650
HUMAN-X2.DNA     601 TTTTCTGGGG TACCTGGCCT GGTGTAAGTG AGGCACACCC TGGTGGCTAC     650
                         660        670        680        690        700
MOUSE-X2.DNA     651 AAGTCCTCCT TCAAACAGGC CAAGATGATG ATTAGGCCCA AGAATTTCAA     700
HUMAN-X2.DNA     651 AAGTCCTCCT TCAAAGAGGC TAAGATGATG ATCAGACCCA AGCACTTTAA     700
                         710        720        730        740        750
MOUSE-X2.DNA     701 GCCATAA... .......... .......... .......... ..........     750
HUMAN-X2.DNA     701 GCCATAA... .......... .......... .......... ..........     750
```

FIGURE 5

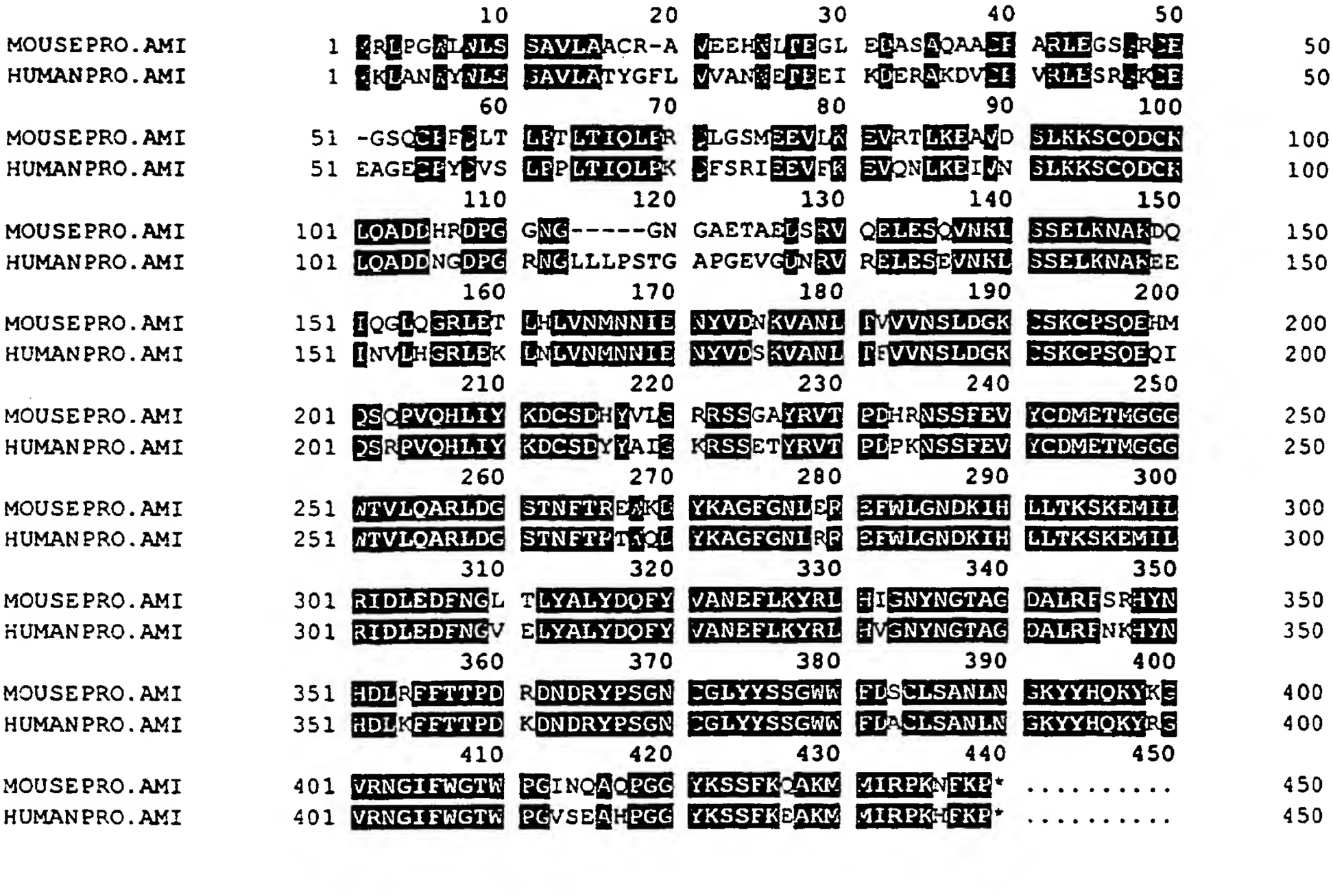

10 20 30 40 50
MOUSEPRO.AMI 1 MRLPGMLVLS SAVLAACR-A MEEHSLTEGL EDASAQAAEF ARLEGSMRCE 50
HUMANPRO.AMI 1 MKLANMYVLS SAVLATYGFL VVANMETEEI KDERAKDVCE VRLESRMKCE 50
60 70 80 90 100
MOUSEPRO.AMI 51 -GSQCEFDLT LPTLTIQLER DLGSMEEVLN EVRTLKEAVD SLKKSCQDCK 100
HUMANPRO.AMI 51 EAGECFYDVS LPPLTIQLPK DFSRIEEVFK EVQNLKEIVN SLKKSCQDCK 100
110 120 130 140 150
MOUSEPRO.AMI 101 LQADLHRDPG GNG-----GN GAETAELSRV QELESQVNKL SSELKNAKDQ 150
HUMANPRO.AMI 101 LQADDNGDPG RNGLLLPSTG APGEVGLNRV RELESEVNKL SSELKNAKEE 150
160 170 180 190 200
MOUSEPRO.AMI 151 IQGLQGRLET LHLVNMNNIE NYVDNKVANL IVVVNSLDGK CSKCPSQEHM 200
HUMANPRO.AMI 151 INVLHGRLEK LNLVNMNNIE NYVDSKVANL IFVVNSLDGK CSKCPSQEQI 200
210 220 230 240 250
MOUSEPRO.AMI 201 QSQPVQHLIY KDCSDHYVLS RRSSGAYRVT PDHRNSSFEV YCDMETMGGG 250
HUMANPRO.AMI 201 QSRPVQHLIY KDCSDYYAIS KRSSETYRVT PDPKNSSFEV YCDMETMGGG 250
260 270 280 290 300
MOUSEPRO.AMI 251 NTVLQARLDG STNFTREMKL YKAGFGNLEP CFWLGNDKIH LLTKSKEMIL 300
HUMANPRO.AMI 251 NTVLQARLDG STNFTPTMQL YKAGFGNLRP CFWLGNDKIH LLTKSKEMIL 300
310 320 330 340 350
MOUSEPRO.AMI 301 RIDLEDFNGL TLYALYDQFY VANEFLKYRL HISNYNGTAG DALRFSRHYN 350
HUMANPRO.AMI 301 RIDLEDFNGV ELYALYDQFY VANEFLKYRL HVSNYNGTAG DALRFNKHYN 350
360 370 380 390 400
MOUSEPRO.AMI 351 HDLRFFTTPD RDNDRYPSGN CGLYYSSGWW FDSCLSANLN GKYYHQKYKS 400
HUMANPRO.AMI 351 HDLKFFTTPD KDNDRYPSGN CGLYYSSGWW FDACLSANLN GKYYHQKYRS 400
410 420 430 440 450
MOUSEPRO.AMI 401 VRNGIFWGTW PGINQAQPGG YKSSFKQAKM MIRPKNFKP* 450
HUMANPRO.AMI 401 VRNGIFWGTW PGVSEAHPGG YKSSFKEAKM MIRPKHFKP* 450

FIGURE 6

```
                          10         20         30         40         50
MOUSEPRO.AMI       1 MRLPGWLWLS SAVLAACR-A VEEHNLTEGL EDASAQAACP ARLEGSGRCE      50
HUMANPRO.AMI       1 MKLANWYWLS SAVLATYGFL VVANNETEEI KDERAKDVCP VRLESRGKCE      50
                          60         70         80         90        100
MOUSEPRO.AMI      51 -GSQCPFQLT LPTLTIQLPR QLGSMEEVLK EVRTLKEAVD SLKKSCQDCK     100
HUMANPRO.AMI      51 EAGECPYQVS LPPLTIQLPK QFSRIEEVFK EVQNLKEIVN SLKKSCQDCK     100
                         110        120        130        140        150
MOUSEPRO.AMI     101 LQADDHRDPG GNG-----GN GAETAEDSRV QELESQVNKL SSELKNAKDQ     150
HUMANPRO.AMI     101 LQADDNGDPG RNGLLLPSTG APGEVGDNRV RELESEVNKL SSELKNAKEE     150
                         160        170        180        190        200
MOUSEPRO.AMI     151 IQGLQGRLET LHLVNMNNIE NYVDNKVANL TVVVNSLDGK CSKCPSQEHM     200
HUMANPRO.AMI     151 INVLHGRLEK LNLVNMNNIE NYVDSKVANL TFVVNSLDGK CSKCPSQEQI     200
                         210        220        230        240        250
MOUSEPRO.AMI     201 QSQPVQHLIY KDCSDHYVLG RRSSGAYRVT PDHRNSSFEV YCDMETMGGG     250
HUMANPRO.AMI     201 QSRPVQHLIY KDCSDYYAIG KRSSETYRVT PDPKNSSFEV YCDMETMGGG     250
                         260        270        280        290        300
MOUSEPRO.AMI     251 WTVLQARLDG STNFTREWKD YKAGFGNLER EFWLGNDKIH LLTKSKEMIL     300
HUMANPRO.AMI     251 WTVLQARLDG STNFTRTWQD YKAGFGNLRR EFWLGNDKIH LLTKSKEMIL     300
                         310        320        330        340        350
MOUSEPRO.AMI     301 RIDLEDFNGL TLYALYDQFY VANEFLKYRL HIGNYNGTAG DALRFSRHYN     350
HUMANPRO.AMI     301 RIDLEDFNGV ELYALYDQFY VANEFLKYRL HVGNYNGTAG DALRFNKHYN     350
                         360        370        380        390        400
MOUSEPRO.AMI     351 HDLRFFTTPD RDNDRYPSGN CGLYYSSGWW FDSCLSANLN GKYYHQKYKG     400
HUMANPRO.AMI     351 HDLKFFTTPD KDNDRYPSGN CGLYYSSGWW FDACLSANLN GKYYHQKYRG     400
                         410        420        430        440        450
MOUSEPRO.AMI     401 VRNGIFWGTW PGINQAQPGG YKSSFKQAKM MIRPKNFKP* ..........     450
HUMANPRO.AMI     401 VRNGIFWGTW PGVSEAHPGG YKSSFKEAKM MIRPKHFKP* ..........     450
```

FIGURE 7

```
          10        20        30        40        50        60        70
     MKLANWYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVSLPPLTIQLPK
HELIX HHhhhhhhhhhhhhhhhhhhhhhHHhhhhHHHHHHHHH                          hh
SHEET   SSSSSSSSSSSsssSSSs                SSSSSS           ssssSSSssssSSsss
TURN                 TTTT      TTTT                TTTTTTT    TTTT   TTTT  TTT
COIL                                     C              CCCC

          80        90        100       110       120       130       140
     QFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELESEVNEL
HELIX hHHHHHHHHHHHHHHHHHHH                                        HHHHHHDH
SHEET sssssssssssssssssss       sSs           sSs
TURN  T                   TTTTTTTTTT TTTTTTTTTTTT TTTTTTTTTTTTT
COIL                                                              CCC

          150       160       170       180       190       200       210
     SSELENAKEEINVLHGRLEKLNLVNHNNIENYVDSKVANLTFVVNSLDGKCSKCPSQEQIQSRPVQHLIY
HELIX   HHHHHHHHHhhhhHhhhhHHhhhhhh          hhhhhhhhhh          hhhhhhhhhhhhhh
SHEET           SSSs      SSSSssssSSSSs   sSSSSSSSSs          sSSSSSSSSSSSs
TURN                TTTT      TTTT    TTTTT        TTTTTTTTTTT            T
COIL  CC

          220       230       240       250       260       270       280
     KDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRR
HELIX h                                  h    hhhhhhhh     hhhH          HHH
SHEET s     sSS      sSSSs       sSSSSSSSs    sSSSSSSs     sSSss
TURN  TTTTTTT  TTTTTTT   TTTTTTTT       TTTTTT      TTTTTT   TTTTT
COIL                                                        CCCCC

          290       300       310       320       330       340       350
     EFWLGNDKIKLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYN
HELIX HHHh    hhhhhhhhhhHhhhhhhhHHhhhhhhhhhhhhhhhhhhhhhhhhH
SHEET ssss    SSSSs     SSSSSSs     SSSSSSSSSSSSSSSSsSSSss
TURN     TTTTT    TTTT         TTTT                    TTTTTTTTTT    TTTTT
COIL                                                        CCCC

          360       370       380       390       400       410       420
     HDLKFFTTPDKDNDRYPSGNCGLYYSSGNWFDACLSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGG
HELIX  hhhhhhh                        hhhhhhH                        hhhHHHh
SHEET  ssSSSSs                 sSs    sSSSSs        sSSSSSSssssSSSSSssss
TURN  TTT    TTTTTTTTTTTTTTT TTTTTT     TTTTTTTT      TTTT     TTTT   TTTT
COIL

          430       440
     YKSSFKEAKMMIRPKHFKP*
HELIX     hhHHHHHHH
SHEET           sss
   N  TTTTTT      TTTT
COIL                 CCC
```

FIGURE 8

```
                          10         20         30         40         50
MOUSEPRO.DNA       1 TCGGTTTGGA TATCATGGGA TG-GAATGAG AAGGGA-AAG TAGGAGCCCG      50
HUMANPRO.DNA       1 TAGGGTTGGA AGCCAGGTCT CCTGAGTATG CGAGAATAAA TACAGTCATG      50
                          60         70         80         90        100
MOUSEPRO.DNA      51 AGAGTGCGGT AAGACAA--G GCATAAGGCG TGTCTGACAA ATTCTTCATA     100
HUMANPRO.DNA      51 GAAGTGTAAA GAGTCTGCCA ACATTTTGAG AATGTGAATA GGATTTGGC-     100
                         110        120        130        140        150
MOUSEPRO.DNA     101 CACACATTTC CCCTTTGCAC ATTCAGTCTG TATAGGTTAT TTCTATAGGA     150
HUMANPRO.DNA     101 TA-AAATTAA GGGGATATAC AGAAAAGTCA TAGGAAATCA GGTTAAAGAC     150
                         160        170        180        190        200
MOUSEPRO.DNA     151 GAAAAAAAAT ATTCAAATTC CTTGTGCACT G-GTAACAGG CATGAAGGCT     200
HUMANPRO.DNA     151 ATAAATATGA GATAGGCTAC AGAGTGTTTT AAGTAATACA ATAAAACATT     200
                         210        220        230        240        250
MOUSEPRO.DNA     201 CAGCAAAGCC AATACGTGTT ATGTCCAGTT GGAGACAGTG CCAGGGCCAA     250
HUMANPRO.DNA     201 TAG--ATTTT TGCCCATGTC A-GTCATTTT GAAATTATTT TTAAAGCAAA     250
                         260        270        280        290        300
MOUSEPRO.DNA     251 CATTCCAGAC TTCTCAGATA GAAAGTGCGC CTGCCTGCCC -TGCTCTGAG     300
HUMANPRO.DNA     251 AAAACC---C TTTTTAAACA AGAAATCTTA TGAGATGTCA ATATGCAAAA     300
                         310        320        330        340        350
MOUSEPRO.DNA     301 --AATTTGAA GAGAGTAGTT C----AGTTA GAATTAAGAG GCAGTAGAGA     350
HUMANPRO.DNA     301 CAAATTAAAA GGAGGTGGTT TCTCTAACTG AAGCTGTTCC TCTTTCCTGC     350
                         360        370        380        390        400
MOUSEPRO.DNA     351 AA--AGTCTT GGGAAATCTG GTTAGAGA-- TATAAATATG AGAACTGGAC     400
HUMANPRO.DNA     351 CTTCAGCCTC TGAAGAGAAA GTTAGAAAAC TATTATCATT AATGCTACAT     400
                         410        420        430        440        450
MOUSEPRO.DNA     401 ATGGTGGTAC ACACCTGTGA TCTCTGTGTT TAGGAGGGAG AGGCAGAGAG     450
HUMANPRO.DNA     401 GTTTTGA-AC AAGCTGATAT ACCAAGTGGC CCAGAGAGC- AGGTAGAAGA     450
                         460        470        480        490        500
MOUSEPRO.DNA     451 ATCAGGAGTT CAAGGCCAGC CTGAGCTACT TGAGACCCAG TCTAAATAAA     500
HUMANPRO.DNA     451 ACCAGCG--- TGGAGACAGA --AAGCAA-- -GAGGCCC-G CCTGCCAGGG     500
                         510        520        530        540        550
MOUSEPRO.DNA     501 TAAGAGATAG ATTACAGAGT GCCTTTAACT AGTACAGAGA AAGAATTTGG     550
HUMANPRO.DNA     501 CTACCTGCAG AA-AGAAAGG GCAAAGATGC TGTAGGCAAG AGAAGTTCAG     550
                         560        570        580        590        600
MOUSEPRO.DNA     551 GTTTATCTGT GTCAGTTACG CTGAAATAAT TTTTAAGTAA TAAAATCCCT     600
HUMANPRO.DNA     551 GACAGACACT GGCA--TA-G CTCAAA-GAT TCACATTTGA GCAG-----C     600
                         610        620        630        640        650
MOUSEPRO.DNA     601 TTTAATAAGA AACCTTATGA G-GTCAGTAT GCACAATGAA CTTAAGAGAG     650
HUMANPRO.DNA     601 TGTGGAAGAT GACAGTACAA TTACCAAAAT GT-CGAAGGG C--AAAGGAG     650
                         660        670        680        690        700
MOUSEPRO.DNA     651 ACCCCCAGCT CCTGAGCTGA GTGATGGGGA AGGACAGCCA CTGCCTGTGA     700
HUMANPRO.DNA     651 GC----AGCT ACTGGTTT-- -TGATG---A AAGACAATTA TGTCCTTT--     700
                         710        720        730        740        750
MOUSEPRO.DNA     701 TGTGTGAGTG ACGTGCTTCC AAGTGTTTTA ACCACTGACG ATTACATAGC     750
HUMANPRO.DNA     701 TAAATGGGTC TTAGACATTT AGACATTTAT AT-AC--ACT ATGCTACGGA     750
                         760        770        780        790        800
MOUSEPRO.DNA     751 CTGCACAGTC AGGAGAAAAC AGCCGTATTC TCTGCCAGTT CTCTTCCCTT     800
HUMANPRO.DNA     751 CAAAGGAAT- AGAAAGTAGC A-CTTTTTTC TCCACTAGTT TTCTTCTCTT     800
                         810        820        830        840        850
MOUSEPRO.DNA     801 TTACAAACAG ATGAGAGACA CACACAGAGA ATCCATTTAA AGAGCGGACC     850
HUMANPRO.DNA     801 TTTCAAGTAG ATGAAGCAAA AGT-CAACTG CAATAGTCAG AAAGCTGTAC     850
                         860        870        880        890        900
```

FIGURE 8 cont'd

```
MOUSEPRO.DNA     851 TTTGTTCTGA TTAGGGGCAA TTTTAAGTAC TTAAGAGTTC ACACAAAGTC  900
HUMANPRO.DNA     851 TTTGTTACAC TTAGAAACTT CTAAAAGTGC TTAAGATTTC ACCTGAAAGT  900
                         910        920        930        940        950
MOUSEPRO.DNA     901 TAGCCTTCAA AAAGAAAACA GGTTCCCAAA ----CTA--- -GGGAGGAAA  950
HUMANPRO.DNA     901 CCAACAT-GA AGAAAATACA GGCTCCCCAA TGCCCCATTC TAAGAAGAAA  950
                         960        970        980        990       1000
MOUSEPRO.DNA     951 CAGAATCATT TCCATTTTGG TGACATTTA- GTGGGAAGAA GCTCACAGAC 1000
HUMANPRO.DNA     951 AAGGACCATT TTCATTTTAG TAACGTTTCT GTTCTATAGA CAGTTTGGAT 1000
                        1010       1020       1030       1040       1050
MOUSEPRO.DNA    1001 ATTTAGACGT TCCAACTCTT TCCCCACTAG TG-------G ACCAAGT-AT 1050
HUMANPRO.DNA    1001 AACTAGCTCT TACTTTTTAT CTTTAAAAAC TGTTTTTCCA GTGAAGTTAC 1050
                        1060       1070       1080       1090       1100
MOUSEPRO.DNA    1051 ATAATATGGT ATCTTTTGGG CACTGGTATT ACAA-CTGTT TTTTAAACAA 1100
HUMANPRO.DNA    1051 GTATAATTAT TTACTTCAAG CG-TAGTATA CCAAATTACT TTAGAAATGC 1100
                        1110       1120       1130       1140       1150
MOUSEPRO.DNA    1101 AAGACTTTCC TTGTGCTTTA CTAAAAAC-C CA-GACGGTG AATCTTGAAT 1150
HUMANPRO.DNA    1101 AAGACTTTTC TTATACTTCA TAAAATACAT TATGAAAGTG AATCTTG--T 1150
                        1160       1170       1180       1190       1200
MOUSEPRO.DNA    1151 ACAATGCGTG GCACCCACGG CAGGCATTCT ATTGTGCATA GTTTTGACTG 1200
HUMANPRO.DNA    1151 TGGCTGTGTA CATTTGACTA TAATAATTTC AATGCATATT ATTTCTATTG 1200
                        1210       1220       1230       1240       1250
MOUSEPRO.DNA    1201 ACAGGAGATG ACAGCATTTG GCTGGCTGCG CTTGCTGAGG ACCCTCTCCT 1250
HUMANPRO.DNA    1201 AGAGTAAGTT ACAGTTTTTG GCAAACTGCG TTTGATGAGG GCTATCTCCT 1250
                        1260       1270       1280       1290       1300
MOUSEPRO.DNA    1251 CCTG-TGTG- GCGTCTGAGA CT-GTGATGC AAATGCGCCC GCCCTTTTCT 1300
HUMANPRO.DNA    1251 CTTCCTGTGC GTTTCTAAAA CTTGTGATGC AAACGCTCCC ACCCTTTCCT 1300
                        1310       1320       1330       1340       1350
MOUSEPRO.DNA    1301 GGGAACTCAG AACGCCTGAG TCAGGCGGCG GTGGCTATTA AAGCG----- 1350
HUMANPRO.DNA    1301 GGGAACACAG AAAGCCTGAC TCAGGCCATG GCCGCTATTA AAGCAGCTCC 1350
                        1360       1370       1380       1390       1400
MOUSEPRO.DNA    1351 ---CCTGGTC AG-----GCT GGGCT-GCCG CACTGCAAGG ATG.......  1400
HUMANPRO.DNA    1351 AGCCCTGCGC ACTCCCTGCT GGGTGAGCAG CACTGTAAAG ATG.......  1400
```

FIGURE 9

```
         10         20         30         40         50
TAGGGTTGGAAGCCAGGTCTCCTGAGTATGCGAGAATAAATACAGTCATG
         60         70         80         90        100
GAAGTGTAAAGAGTCTGCCAACATTTTGAGAATGTGAATAGGATTTGGCT
        110        120        130        140        150
AAAATTAAGGGGATATACAGAAAAGTCATAGGAAATCAGGTTAAAGACAT
                          TCF1       PEA3
        160        170        180        190        200
AAATATGAGATAGGCTACAGAGTGTTTTAAGTAATACAATAAAACATTTA
          GATA1                   NF IL6
        210        220        230        240        250
GATTTTTGCCCATGTCAGTCATTTTGAAATTATTTTTAAAGCAAAAAAAC
                                NF IL6
        260        270        280        290        300
CCTTTTTAAACAAGAAATCTTATGAGATGTCAATATGCAAAACAAATTAA

        310        320        330        340        350
AAGGAGGTGGTTTCTCTAACTGAAGCTGTTCCTCTTTCCTGCCTTCAGCC
TCF1
        360        370        380        390        400
TCTGAAGAGAAAGTTAGAAAACTATTATCATTAATGCTACATGTTTTGAA
                              NF_E1
        410        420        430        440        450
CAAGCTGATATACCAAGTGGCCCAGAGAGCAGGTAGAAGAACCAGCGTGG
                 bHLH
        460        470        480        490        500
AGACAGAAAGCAAGAGGCCCGCCTGCCAGGGCTACCTGCAGAAAGAAAGG
                                        NF IL6
        510        520        530        540        550
GCAAAGATGCTGTAGGCAAGAGAAGTTCAGGACAGACACTGGCATAGGTC
 TCF1
        560        570        580        590        600
AAAAGATTCACATTTGAGCAGCTGTGGAAGATGACAGTACAATTACCAAAA
TCF1          bHLH    bHLH
                      E2A
        610        620        630        640        650
TGTCGAAGGGCAAAGGAGGCAGCTACTGGTTTTGATGAAAAGACAATTATG
              TCF1                      NF IL6
        660        670        680        690        700
TCCTTTTAAATGGGTCTTAGACATTTAGACATTTATATACACTATGCTAC
        710        720        730        740        750
GGACAAAGGAATAGAAAGTAGCACTTTTTTCTCCACTAGTTTTCTTCTCT
    TCF1
        760        770        780        790        800
TTTTCAAGTAGATGAAGCAAAAGTCAACTGCAATAGTCAGAAAGCTGTAC
                       TCF1     bHLH
```

FIGURE 9 CONT'D

```
          810         820         830         840         850
TTTGTTACACTTAGAAACTTCTAAAAGTGCTTAAGATTTCACCTGAAACG
                              TCF1                  bHLH
          860         870         880         890         900
CCAACATGAAGAAAATACAGGCTCCCCAATGCCCCATTCTAAGAAGAAAA
          910         920         930         940         950
AGGACCATTTTCATTTTAGTAACGTTTCTGTTCTATAGACAGTTTGGATA
          960         970         980         990        1000
ACTAGCTCTTACTTTTTATCTTTAAAAACTGTTTTTCCAGTGAAGTTACG
         1010        1020        1030        1040        1050
TATAATTATTTACTTCAAGCGTAGTATACCAAATTACTTTAGAAATGCAA
                                                NF IL6
         1060        1070        1080        1090        1100
GACTTTTCTTATACTTCATAAAATACATTATGAAAGTGAATCTTGTTGGC
                                  NF IL6
         1110        1120        1130        1140        1150
TGTGTACATTTGACTATAATAATTTCAATGCATATTATTTCTATTGAGAG
          bHLH
         1160        1170        1180        1190        1200
TAAGTTACAGTTTTTGGCAAACTGCGTTTGATGAGGGCTATCTCCTCTTC
         1210        1220        1230        1240        1250
CTGTGCGTTTCTAAAACTTGTGATGCAAACGCTCCCACCCTTTCCTGGGA
                              AABS
            1260        1270        1280        1290        1300
ACACAGAAACGCTGACTCAGGCACGTGCCGCTATTAAAGCAGCTCCAGCC
     +1          AP 1        bHLH        TATA box
            1310        1320        1330
CTGCGCACTCCCTGCTGGGTGAGCAGCACTGTAAAGATG
```

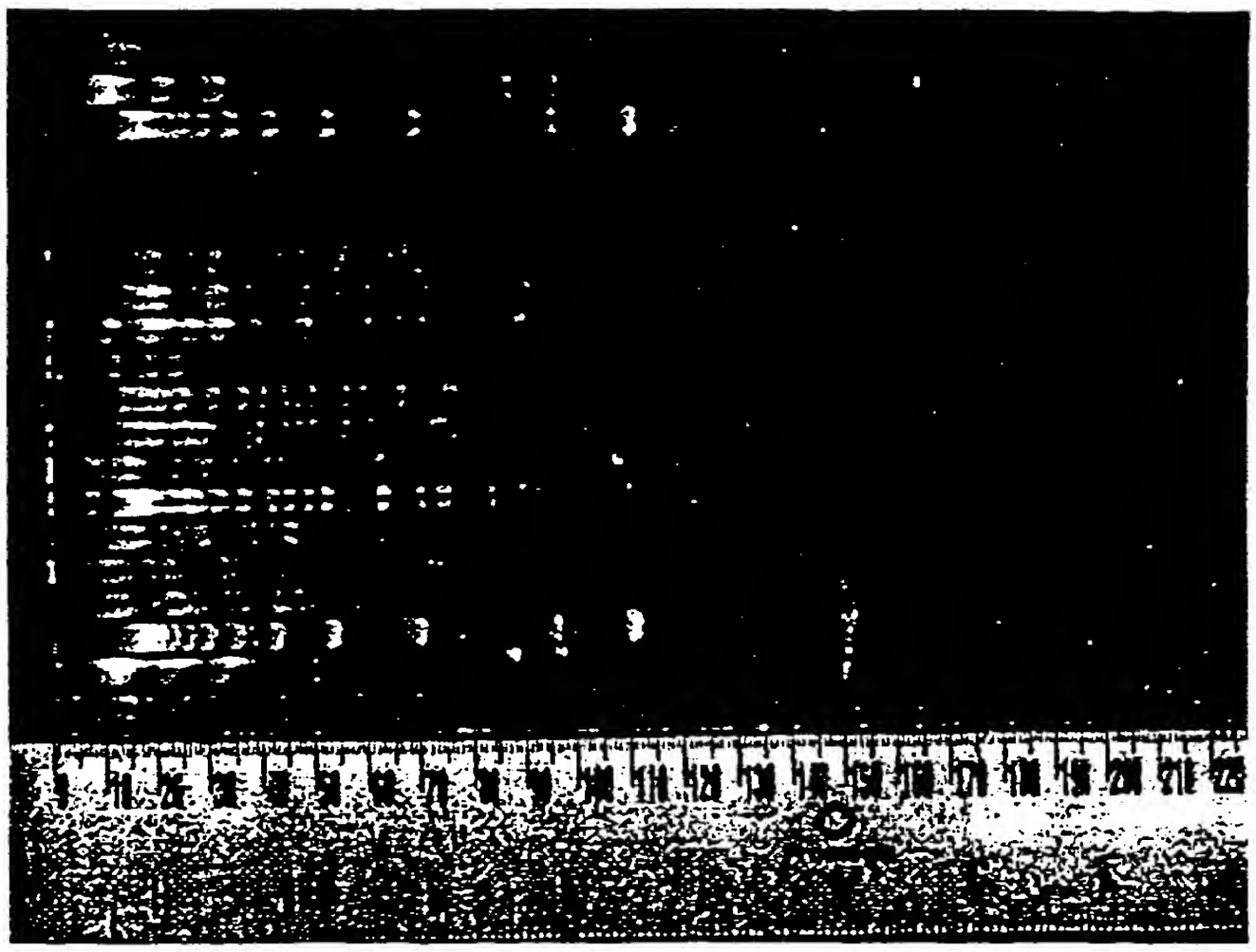


FIGURE 10B

FIGURE 10A

FIGURE 11

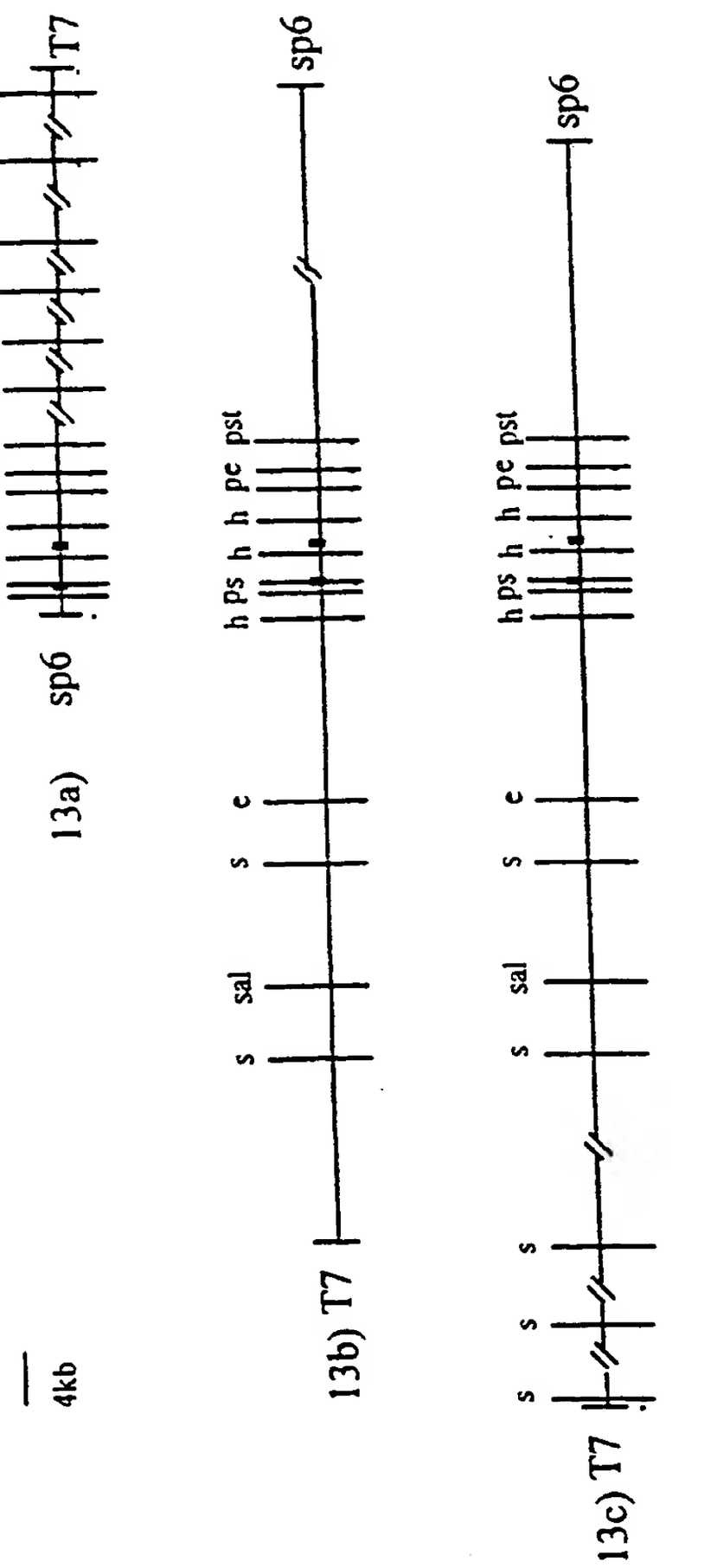

13a)
sp6
ps h h pe pst s s s s s
T7
h ps h h pe pst
sp6
s sal s e
13b) T7
h ps h h pe pst
sp6
s sal s e
s s s
13c) T7
4kb

FIGURE 12

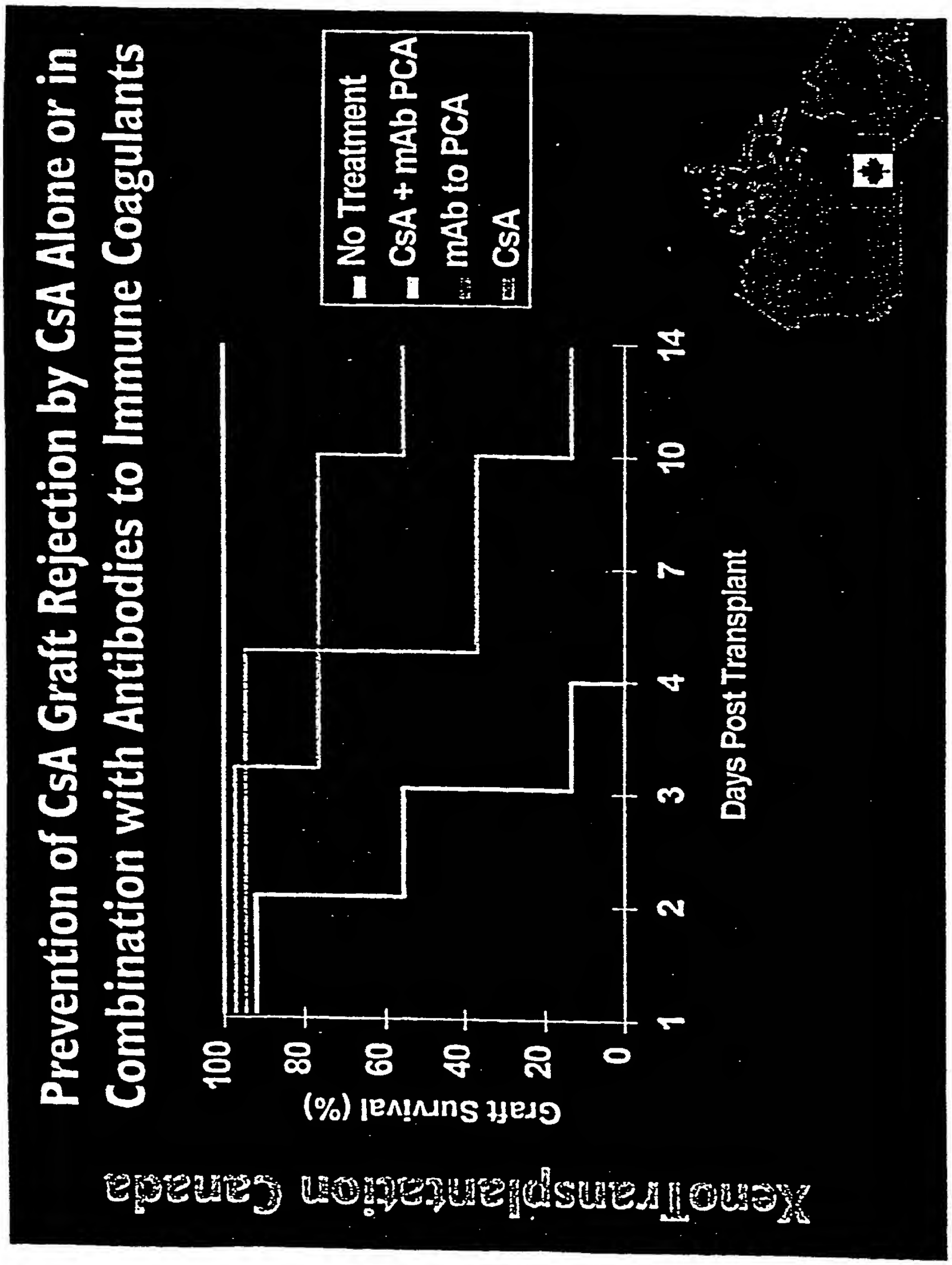

Prevention of CsA Graft Rejection by CsA Alone or in Combination with Antibodies to Immune Coagulants
No Treatment
CsA + mAb PCA
mAb to PCA
CsA
Graft Survival (%)
100
80
60
40
20
0
1
2
3
4
7
10
14
Days Post Transplant
Xenotransplantation Canada

FIGURE 13

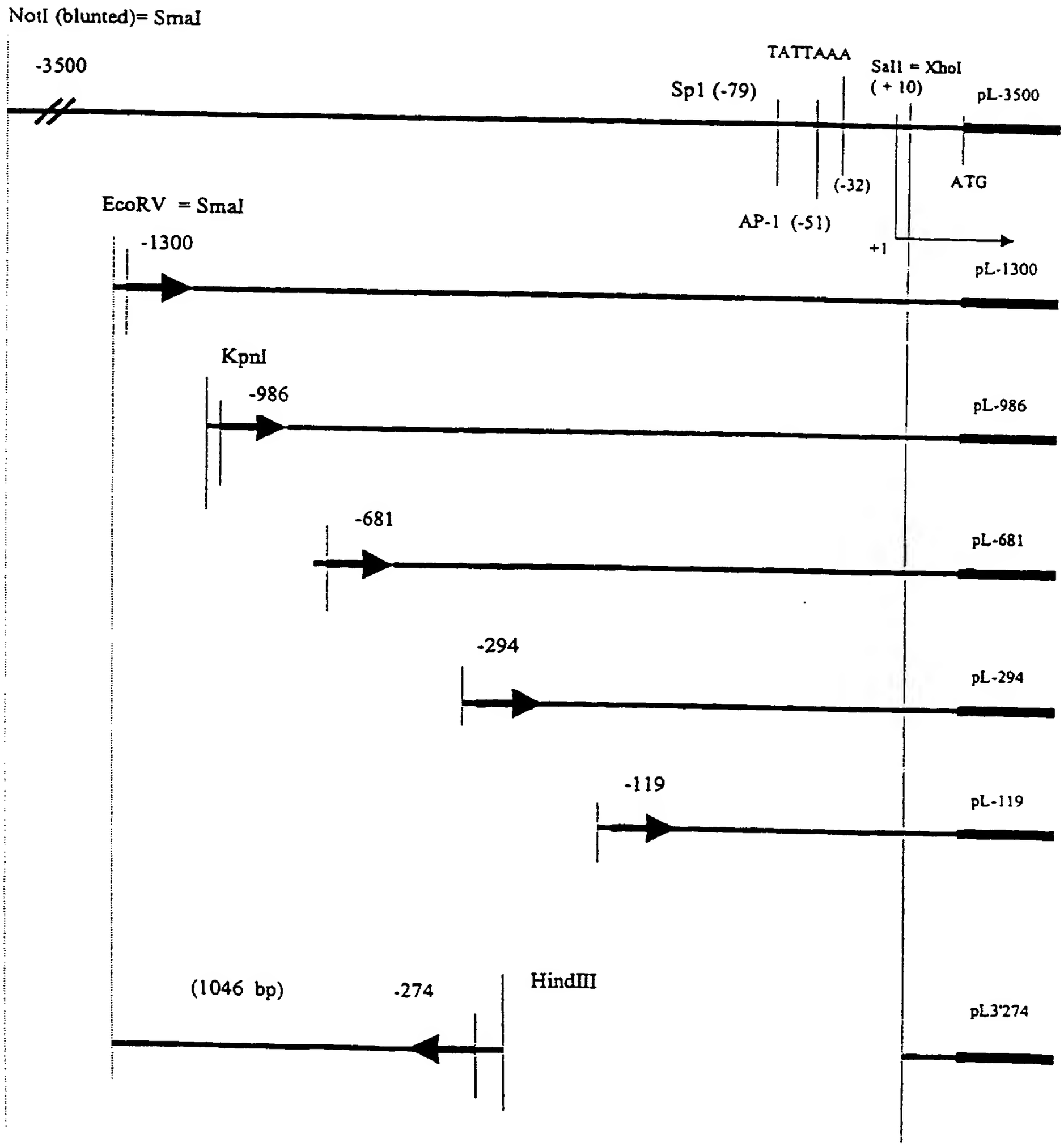

NotI (blunted)= SmaI
-3500
TATTAAA
SalI = XhoI
(+ 10)
Sp1 (-79)
pL-3500
(-32)
ATG
AP-1 (-51)
EcoRV = SmaI
-1300
+1
pL-1300
KpnI
-986
pL-986
-681
pL-681
-294
pL-294
-119
pL-119
(1046 bp)
-274
HindIII
pL3'274

FIGURE 15

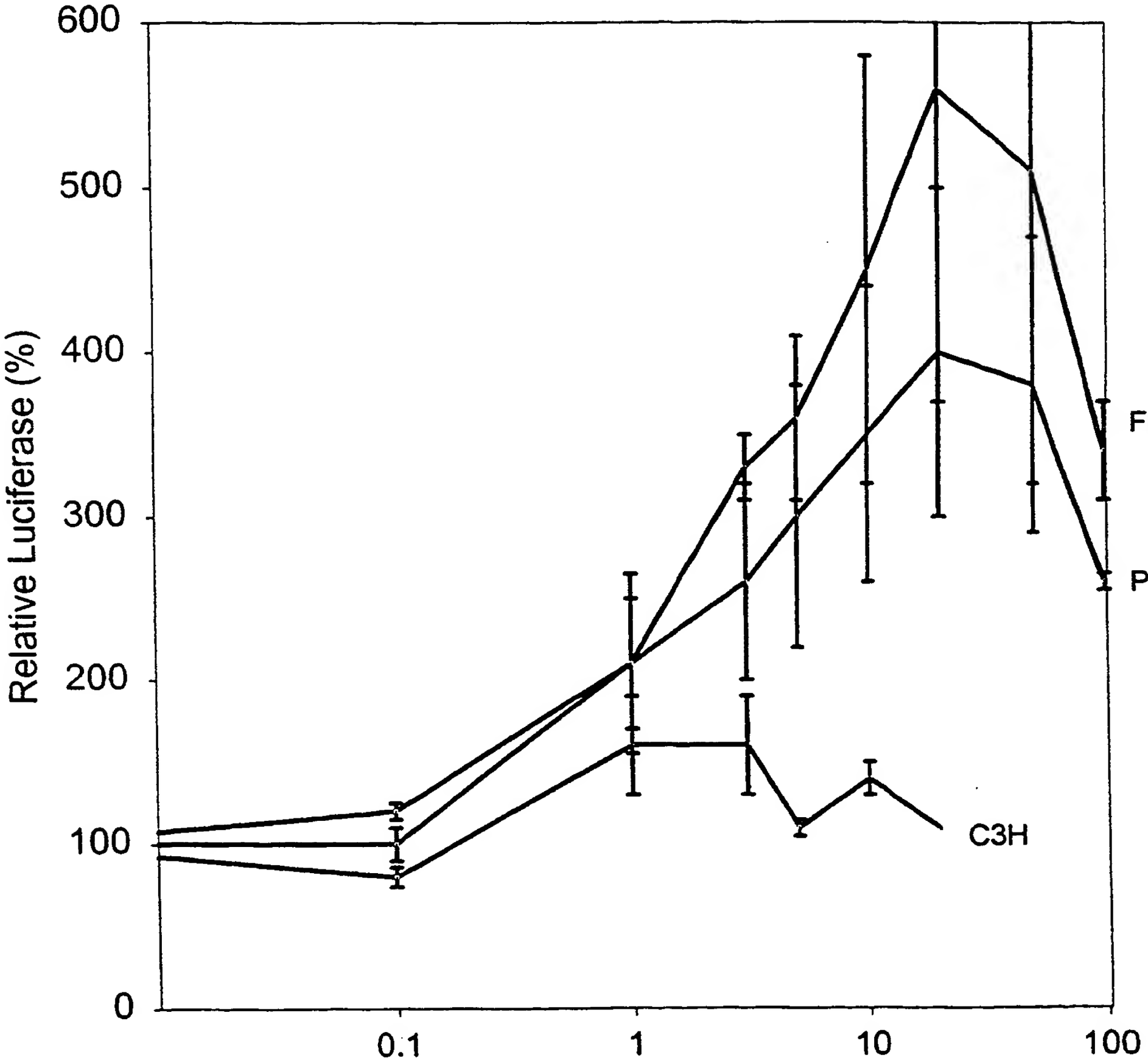

600
500
400
300
200
100
0
Relative Luciferase (%)
0.1
1
10
100
Serum Concentration (%)
FBS
PIG
C3H

FIGURE 16

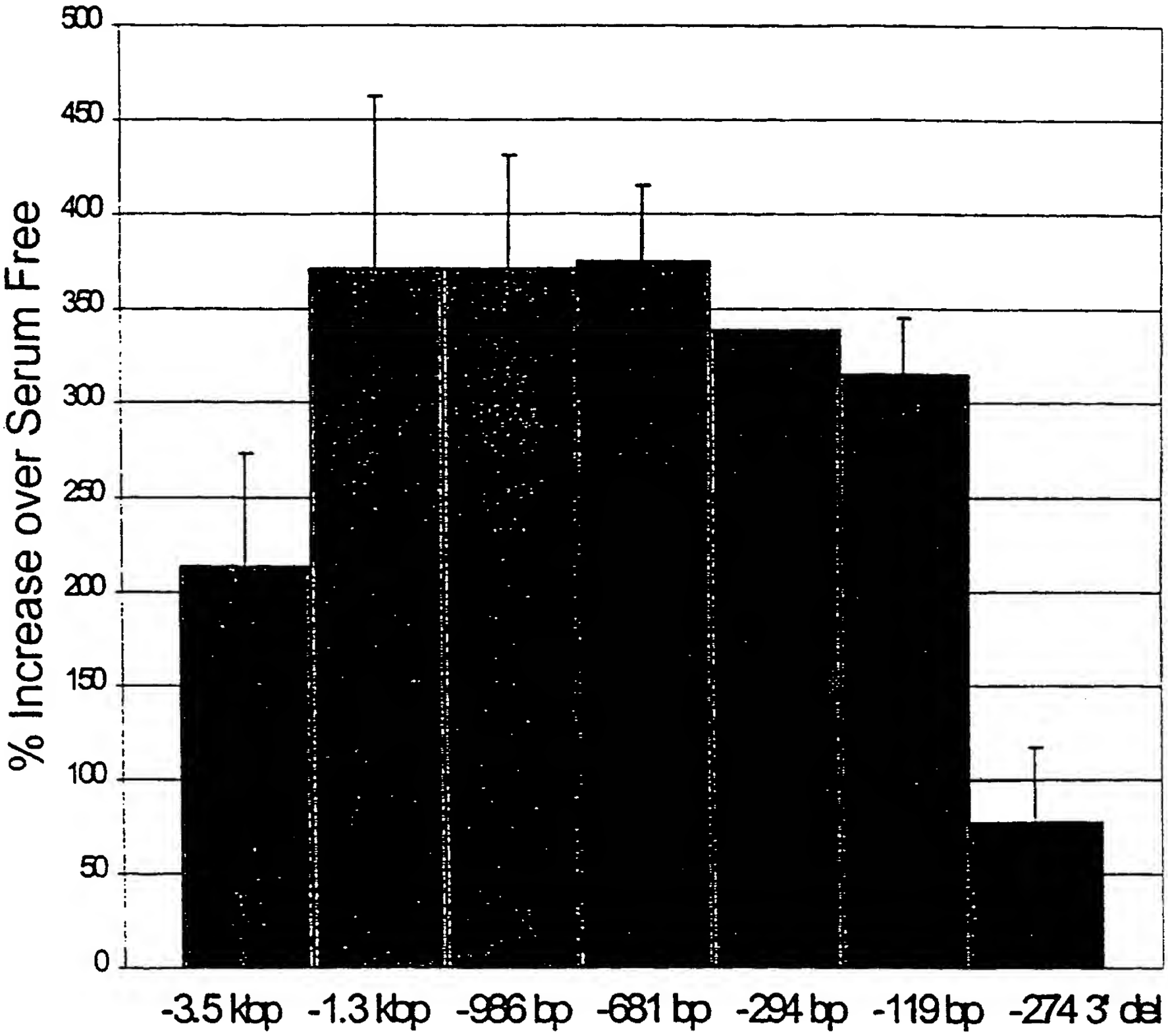

500
450
400
350
300
250
200
150
100
50
0
% Increase over Serum Free
-3.5 kbp
-1.3 kbp
-986 bp
-681 bp
-294 bp
-119 bp
-274 3' del

FIGURE 18

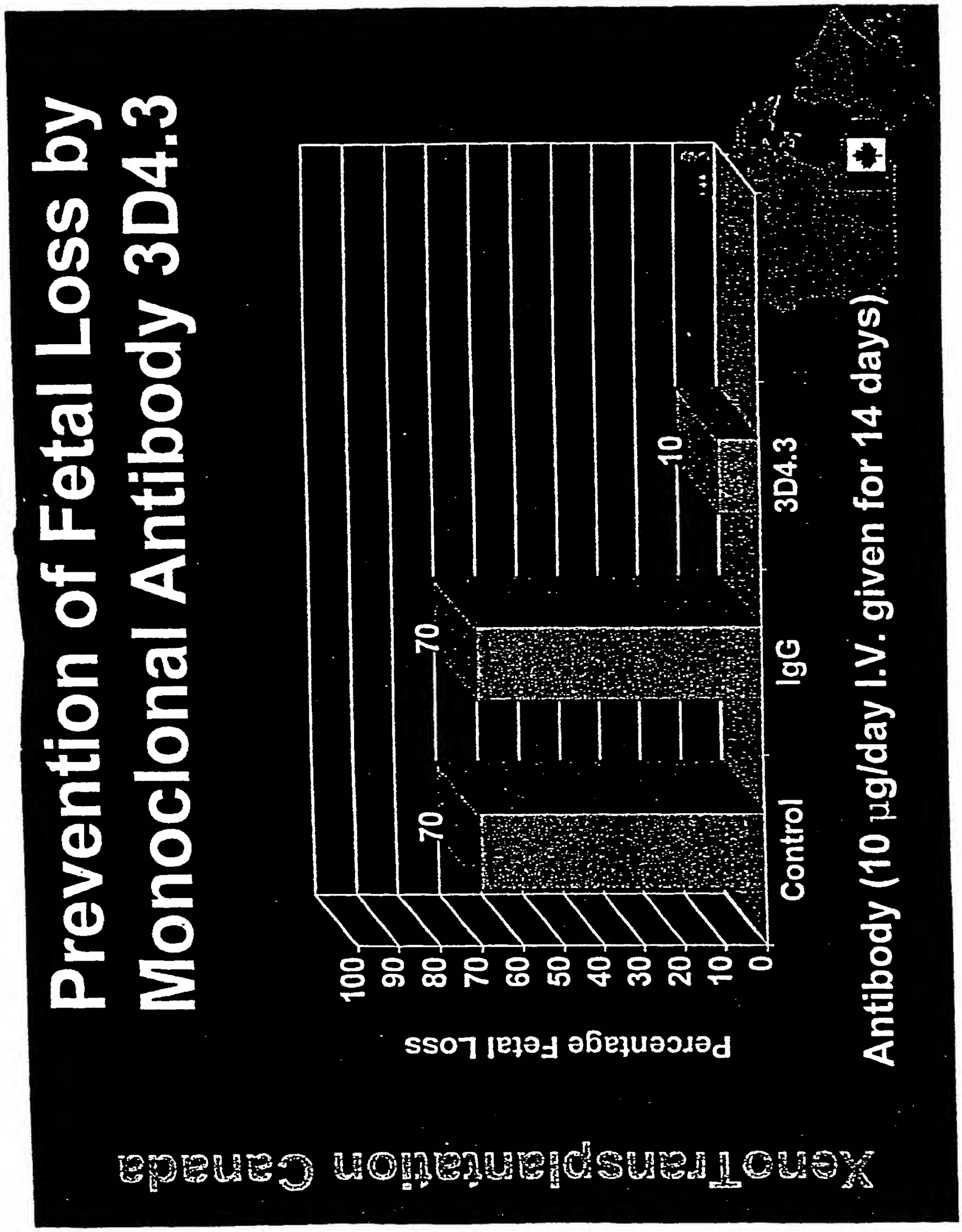

Prevention of Fetal Loss by
Monoclonal Antibody 3D4.3
Xeno Transplantation Canada
Percentage Fetal Loss
100
90
80
70
60
50
40
30
20
10
0
Control IgG
70
70
10
3D4.3
Antibody (10 µg/day I.V. given for 14 days)

FIGURE 19

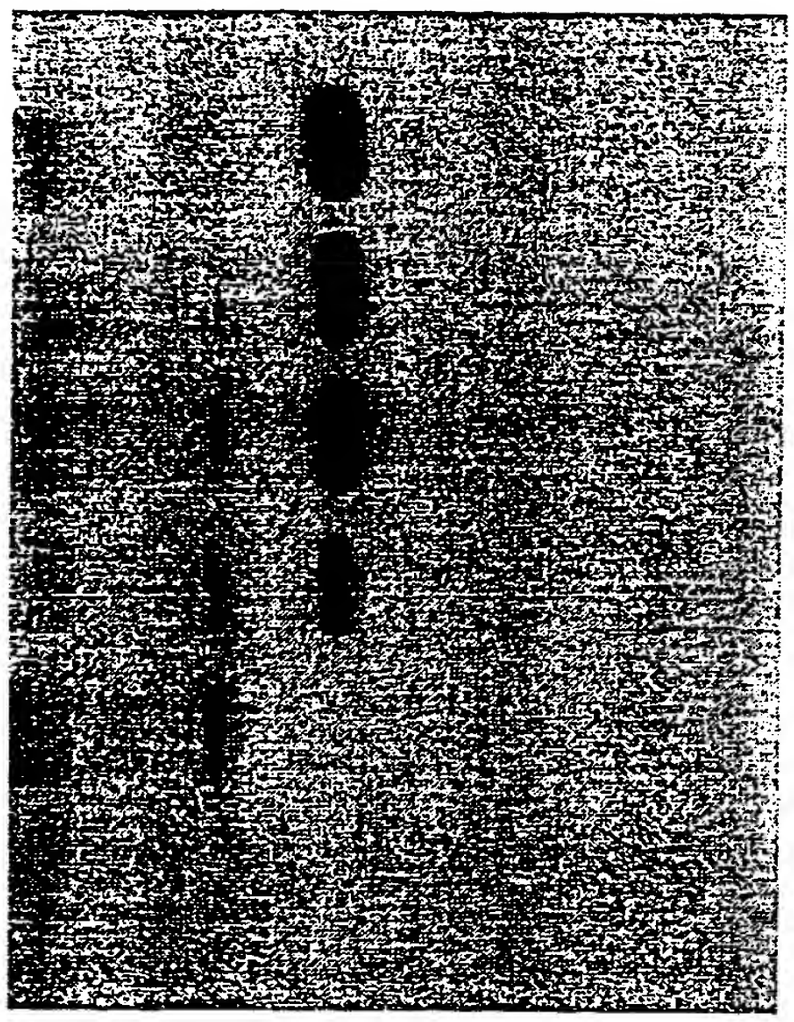
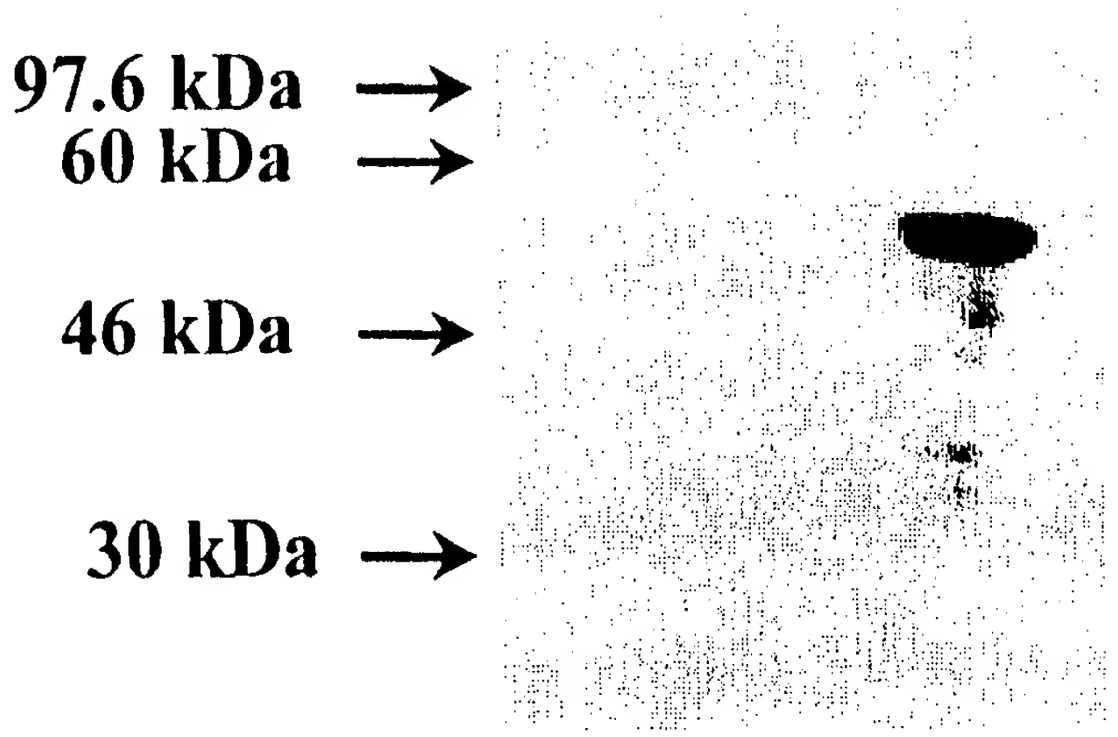

Time post infection
0 12 24 48 72 96 120 h
97.6 kDa
60 kDa
46 kDa
30 kDa

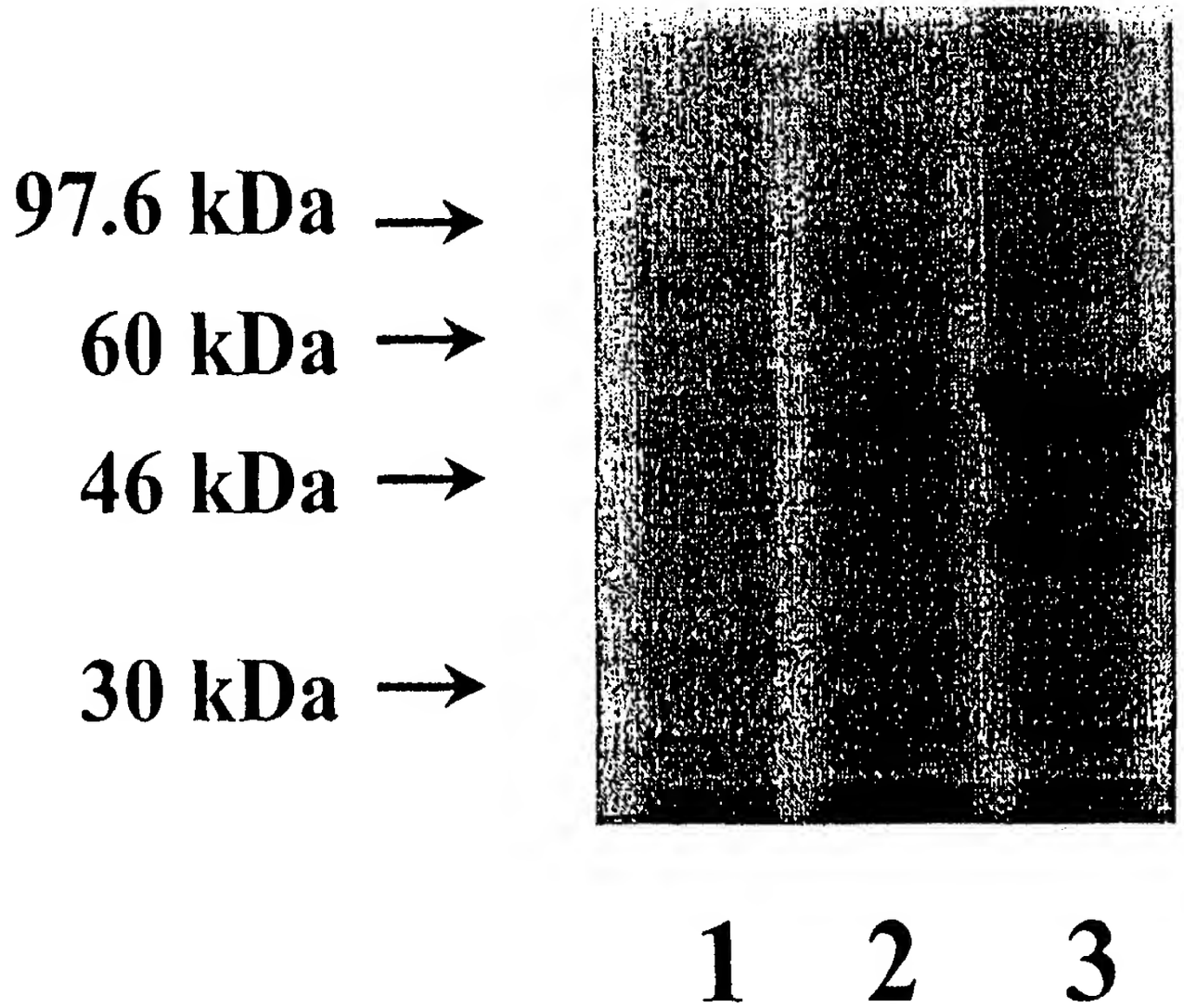
FIGURE 20



The lanes are:

1. H5cells
2. H5 + wild type virus
3. H5 + recombinant virus

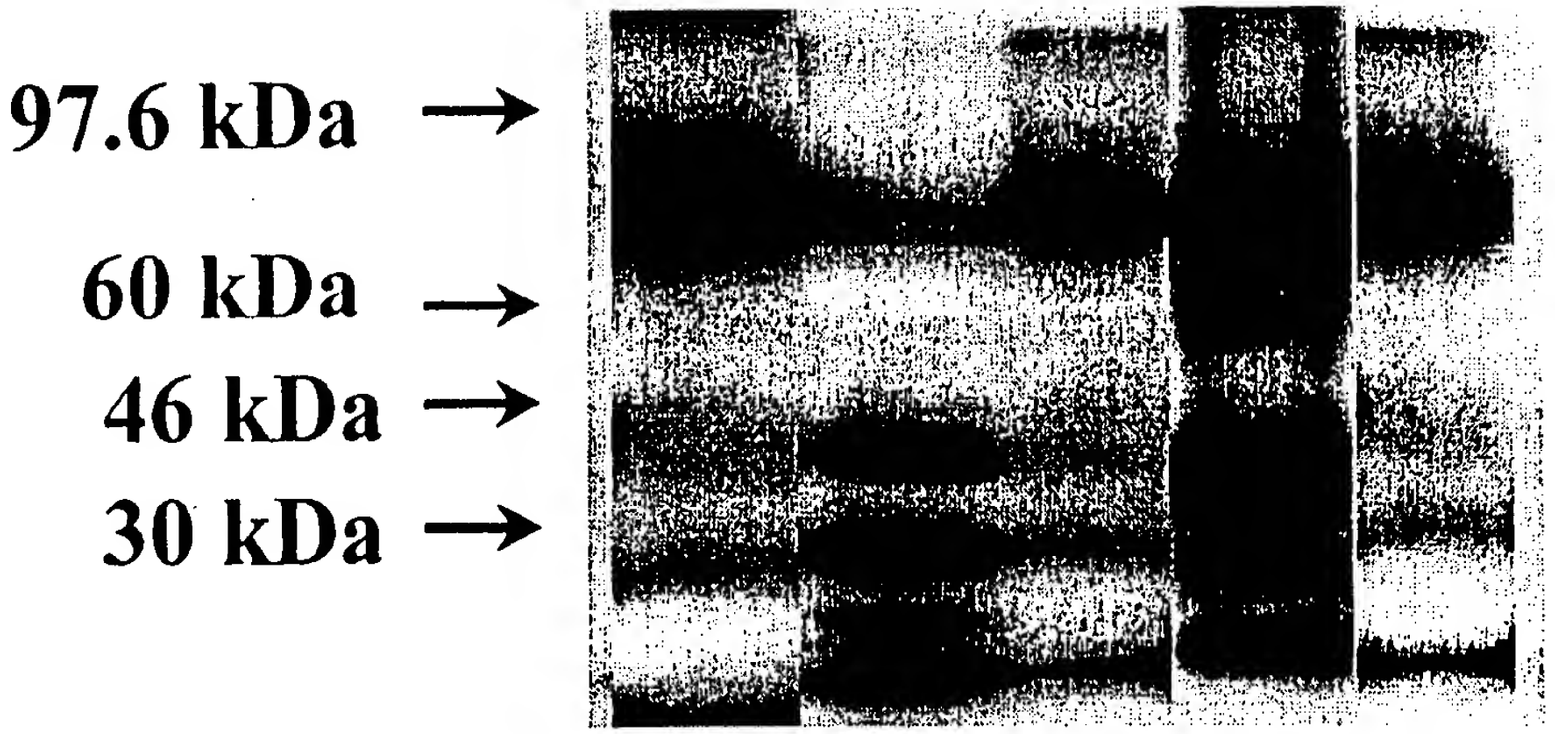
FIGURE 21



The lanes are:

1. H5cells
2. H5 + wild type virus
3. H5 + recombinant virus

FIGURE 22



The lanes are:

1. ^{125}I-Prothrombin (PT)
2. PT +RVV + Factor X
3. PT +H5
4. PT + H5-RV
5. PT + purified protein (3 µg)